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IN THE CLAIMS

Please cancel claims 3-4, 12 and 24-30.

Please amend the remaining claims as follows:

1. (Amended) An isolated or purified [Oligonucleotide]oligonucleotide for the specific identification of *Staphylococci* species, comprising [having] a nucleotide sequence [comprising between]of about 15 [and]to 350 base pairs[, preferably between 17 and 250 base pairs, and which presents less than 50% homology with] of the "consensus" *femA* nucleotide sequence [(CNS) of Fig. 3]SEQ ID NO:1.

2. (Amended) The [Oligonucleotide]oligonucleotide according to claim 1 [for the specific identification of *Staphylococci* species having]comprising a nucleotide sequence [comprising between 15 and 350 base pairs, preferably between]of about 17 [and]to 250 base pairs[, and which presents less than 40% homology with]of [the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3]SEQ ID NO:1.

5. (Amended) The [Oligonucleotide]oligonucleotide according to claim 1, [being a primer which]wherein the nucleotide sequence [has between]comprises about 15 [and]to 45 base pairs[, preferably between 17 and 25 base pairs].

6. (Amended) The [Oligonucleotide]oligonucleotide according to Claim 5, which is selected from the group consisting of [the following nucleotide sequences:

- ACAGCAGATGACATCATT
- TAATGAAAGAAATGTGCTTA
- ACACAACTTCAATTAGAAC
- AGTATTAGCAAATGCGG
- ATGCATATTTTCCGTAA
- CAGCAGATGACATCATT
- CATCTAAAGATATATTAAATGGA
- AGTATTAGCAAATGCGGGTCAC
- CAACACAACTTCAATTAGAA] SEQ ID NOS:45-53.

7. (Amended) [Couple of]Two or more isolated or purified oligonucleotides for the specific amplification of *Staphylococci* species [consisting of]comprising [two different]at least one nucleotide sequence[s having between] of about 15 [and]to 45 base pairs[, preferably between 17 and 25 base pairs, and which present] more than 60% [homology with]homologous to [the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3]SEQ ID NO:1 and/or [consisting of one nucleotide sequence] at least one oligonucleotide [having

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between] about 15 [and] to 45 base pairs[, preferably between 17 and 25 base pairs, and which presents] more than 60% [homology with] homologous to [the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3 and the oligonucleotide of Claim 6] SEQ ID NOS:1, and 45-53.

8. (Amended) [Couple of] The oligonucleotides according to Claim [1 for the specific amplification of *Staphylococci* species, consisting of two different nucleotide sequences having between 15 and 45 base pairs, preferably between 17 and 25 base pairs, and which present more than 70% homology with the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3 or consisting of one nucleotide sequence having between 15 and 45 base pairs, preferably between 17 and 25 base pairs, and which presents more than 70% homology with the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3 and the oligonucleotide of Claim 1] 7 wherein said oligonucleotides have more than 70% homology to SEQ ID NOS:1, and 45-53.

9. (Amended) [Couple of] The oligonucleotides according to Claim [7 or 8 for the specific amplification of *Staphylococci* species, consisting of two different nucleotide sequences having between 15 and 45 base pairs, preferably between 17 and 25 base pairs, and which present more than 80% homology with the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3 or consisting of one nucleotide sequence (CNS) of Fig. 3 or consisting of one nucleotide sequence having between 15 and 45 base pairs, preferably between 17 and 25 base pairs, and which presents more than 80% homology with the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3 and the oligonucleotide of Claim 1] 8 wherein said oligonucleotides have more than 80% homology to SEQ ID NOS:1, and 45-53.

10. (Amended) [Couple of] The oligonucleotides according to [any one of the Claims 7 to 9 for the specific amplification of *Staphylococci* species, consisting of two different nucleotide sequences having between 15 and 45 base pairs, preferably between 17 and 25 base pairs, and which present more than 90% homology with the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3 or consisting of one nucleotide sequence having between 15 and 45 base pairs, preferably between 17 and 25 base pairs, and which presents more than 90% homology with the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3 and the oligonucleotide of Claim 1] Claim 9 wherein said oligonucleotides have more than 90% homology to SEQ ID NOS:1, and 45-53.

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11. (Amended) [Couple of] The oligonucleotides according to [any one of the Claims 7 to 10, wherein the oligonucleotides having between 15 and 45 base pairs, preferably between 17 and 25 base pairs, and which present more than 60, 70, 80 or 90% homology with the "consensus" *femA* nucleotide sequence (CNS) of Fig. 3 are] Claim 7 wherein said oligonucleotides are selected from the group consisting of [the following nucleotide sequences:

- ANAATGAANTTTACNAATTTNACNGCNANAGANTT
and more particularly TAATGAAGTTTACAAAATTT or
TAATGAAGTTTACNAAATTT
- ATGNCNNANAGNCATTTNACNCANA
and more particularly TGCCATATAGTCATTTACGC
- TAGTNGGNATNAANAANAANNATAANGANGTNATTGC
- GTNCCNGTNATGAAANTNTTNAANTANTTTTATTC
- AATGCNGGNNANGATTGG
- GNAANNGNAANACNAAAAAAGTNNANAANAATGGNGTNAAAGT
and more particularly AAAAAGTTCAAAAAATGG and
AAAAAGTACAAAAATGG
- AAGANGANNTNCCNATNTTNGNTCATTNATGGANGATAC
- TATATNNANTTTGATGANTA
- AANGANATNGANAAANGNCCNGANAANAAAAA
and more particularly AAAGATATTGAAAAACGA,
AAAGATATTGAAAAGAGACC, AAAGATATCGAGAAAGAC and
AAAGACATCGACAAGCGT.
- ANCATGGNAANGAATTACCNAT
and more particularly GAACATGGTAATGAATTAC
- AATCCNTNTGAAGTNGTNTANTANGCNGGTGG
- AGNTATGCNNTNCAATGGNNATGATTAANTATGC
- TTTANNGANGANGCNGAAGATGNNGGNGTNNNTNAANTTNAAAAA
and more particularly TTTACTGAAGATGCTGAAGA
- GTTGGNGANTTNNTNAAACC
and more particularly GTTGGTGACTTTATTAAACC
- ATGAAATTTACAGAGTTAA] SEQ ID NOS:18-44.

13. (Amended) A method of [Identification] identification and/or quantification [method] of a *Staphylococci* species, which may present resistance to antibiotics and which is present in a sample, said method comprising the steps of:

- [—] obtaining a nucleotide sequence from a *Staphylococci* species present in the sample,
- [—] amplifying said nucleotide sequence with the [couple of] oligonucleotides according to [any one of the Claims 7 to 11] Claim 7, and
- [—] identifying and/or [possibly] quantifying the specific *Staphylococci* species:

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[—] by reverse hybridization of the amplified nucleotide sequence with one or more oligonucleotide(s) [according to any one of the Claims 1 to 6]having a nucleotide sequence comprising about 15 to 350 base pairs of SEQ ID NO:1, [which is (are)] specific of said *Staphylococci* species [and is (are)]wherein said nucleotide sequence is immobilized on a solid support or
[—] by a comparative measure of the length of the amplified nucleotide sequence.

14. (Amended) [Diagnostic] A diagnostic device for the identification of *Staphylococci* species comprising: [the]an oligonucleotide having a nucleotide sequence comprising about 15 to 350 base pairs of SEQ ID NO:1, and/or the [couple of]two or more oligonucleotides according to [any one of the preceding Claims 1 to 11]Claim 7 [and possibly all the media necessary for the identification of an amplified sequence of said *Staphylococci* species through any one of the methods selected from the group consisting of in situ hybridization, hybridization on a solid support, in solution on dot blot, Northern blot, Southern blot, probe hybridization by the use of an isotopic or non-isotopic label, genetic amplification or a mixture thereof].

15. (Amended) An isolated or purified *femA* [genetic sequence which presents]polynucleotide more than 90% [homology with a]homologous to the nucleotide [or amino acid] sequence selected from the group consisting of [the sequence SEQ ID NO 40, SEQ ID NO 41, SEQ ID NO 42, SEQ ID NO 43, SEQ ID NO 44, SEQ ID NO 45, SEQ ID NO 46, SEQ ID NO 47, SEQ ID NO 48, SEQ ID NO 49, SEQ ID NO 50, SEQ ID NO 51, SEQ ID NO 52, SEQ ID NO 53 and SEQ ID NO 54]SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, and 16.

16. (Amended) [Genetic sequence] The isolated or purified *femA* polynucleotide according to Claim [14, being the nucleotide sequence SEQ ID NO 40]15, wherein said polynucleotide comprises SEQ ID NO:2.

17. (Amended) [Genetic sequence] The isolated or purified *femA* polynucleotide according to Claim [14, being the nucleotide sequence SEQ ID NO 41]15, wherein said polynucleotide comprises SEQ ID NO:4.

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18. (Amended) [Genetic sequence] The isolated or purified *femA* polynucleotide according to Claim [14, being the nucleotide sequence SEQ ID NO 42]15, wherein said polynucleotide comprises SEQ ID NO:6.

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19. (Amended) [Genetic sequence] The isolated or purified *femA* polynucleotide according to Claim [14, being the nucleotide sequence SEQ ID NO 43]15, wherein said polynucleotide comprises SEQ ID NO:8.

20. (Amended) [Genetic sequence] The isolated or purified *femA* polynucleotide according to Claim [14, being the nucleotide sequence SEQ ID NO 44]15, wherein said polynucleotide comprises SEQ ID NO:10.

21. (Amended) [Genetic sequence] The isolated or purified *femA* polynucleotide according to Claim [14, being the nucleotide sequence SEQ ID NO 45]15, wherein said polynucleotide comprises SEQ ID NO:12.

22. (Amended) [Genetic sequence] The isolated or purified *femA* polynucleotide according to Claim [14, being the nucleotide sequence SEQ ID NO 46]15, wherein said polynucleotide comprises SEQ ID NO:14.

23. (Amended) [Genetic sequence] The isolated or purified *femA* polynucleotide according to Claim [14, being the nucleotide sequence SEQ ID NO 47]15, wherein said polynucleotide comprises SEQ ID NO:16.

Please add the following Claims:

31. The oligonucleotide of Claim 5 wherein said sequence comprises about 17 to 25 base pairs.

32. The oligonucleotides according to Claim 7 wherein said nucleotide sequence comprises about 17 to 25 base pairs.

33. The diagnostic device of Claim 14 further comprising all of the media necessary for the identification of an amplified sequence of said *Staphylococci* species through any one of the methods selected from the group consisting of: *in situ* hybridization, hybridization on a solid support, hybridization in solution, hybridization on a dot blot, Northern blot, Southern blot, probe hybridization by the use of an isotopic label, probe hybridization by the use of a non-isotopic label, genetic amplification and a mixture thereof.

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34. An isolated or purified *femA* polypeptide more than 90% homologous to the amino acid sequence selected from the group consisting of SEQ ID NOS: 3, 5, 7, 9, 11, 13, 15, and 17.

35. The isolated or purified *femA* polypeptide according to Claim 34, wherein said polypeptide comprises SEQ ID NO:3.

36. The isolated or purified *femA* polypeptide according to Claim 34, wherein said polypeptide comprises SEQ ID NO:5.

37. The isolated or purified *femA* polypeptide according to Claim 34, wherein said polypeptide comprises SEQ ID NO:7.

38. The isolated or purified *femA* polypeptide according to Claim 34, wherein said polypeptide comprises SEQ ID NO:9.

39. The isolated or purified *femA* polypeptide according to Claim 34, wherein said polypeptide comprises SEQ ID NO:11.

40. The isolated or purified *femA* polypeptide according to Claim 34, wherein said polypeptide comprises SEQ ID NO:13.

41. The isolated or purified *femA* polypeptide according to Claim 34, wherein said polypeptide comprises SEQ ID NO:15.

42. The isolated or purified *femA* polypeptide according to Claim 34, wherein said polypeptide comprises SEQ ID NO:17.

REMARKS

The specification has been amended to include a reference to the International Application No. of the present application, PCT/BE98/00141, filed September 28, 1998 and to assign Sequence Identification Numbers to the sequences disclosed in the Application.

Claims 3-4, 12, and 24-30, have been cancelled. Claims 31-42 have been added. The claims have been amended to more precisely claim the invention according to conventional practice before the United States Patent and Trademark Office.

As a result of the amendments made herein, Claims 1-2, 5-11, 13-23 and 31-42 are presented for examination. No new matter is being added herewith.

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Conclusion

Should there be any questions concerning this application, the Examiner is respectfully invited to contact the undersigned attorney at the telephone number appearing below

Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410. A duplicate copy of this sheet is enclosed.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated:

17 March 2000

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